



No new matter has been added with this amendment.

Claims 11-31 have been cancelled without prejudice. Applicants reserve the right to file a division and/or continuation on the cancelled subject matter.

**Rejection under 35 U.S.C. § 102(b)**

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by WO96/08582. The Examiner states that the cited reference discloses *S. epidermidis* primers. This rejection, to the extent that it applies to the claims as amended is respectfully traversed.

To anticipate a claim under 35 U.S.C. § 102 (b), the reference must contain all of the elements of the claimed limitations. WO 96/08582 contains 4 primers that consist of no more than 25 to 30 nucleotides. Claims 9 and 10 as amended claim a probe or isolated nucleotide sequence that comprises at least 40 nucleotides of the SEQ ID NO:1835. Claim 5 also has been amended to obviate the alleged rejection. Thus WO 96/08582 does not anticipate the claimed invention.

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by U.S. Patent No. 5,770,375 ('375 patent). The Examiner identifies Example 2 and 3 of the '375 patent as containing *S. epidermidis* primers which correlate to SEQ ID NO:5 – SEQ ID NO:8 of the '375 patent. The Applicants have provided the Examiner Exhibits A-D describing with sequence alignments between the claimed sequence SEQ ID NO:1835 and SEQ ID NO:5 – SEQ ID NO:8 disclosed in the Patent '375. As shown in Exhibits A-D detailing the alignments, the sequence overlaps do not exceed 20 bases. Moreover, the amended claims providing the number of nucleotide bases as 40 bases in claims 9 and 10 and the number the 10 amino acids of claim 5, overcome the alleged rejection under 35 U.S.C. § 102 (b).

Withdrawal of these rejections is respectfully requested.



**Conclusion**

Reconsideration and withdrawal of the pending rejections are respectfully requested and a Notice of Allowance is earnestly solicited.

If the Examiner feels that a telephone conference would expedite prosecution of this application, he is invited to call the undersigned at 781-398-2300.

Any deficiency or overpayment for this reply should be charged or credited to Deposit Account No. 50-1040. One duplicate copy of this letter is enclosed.

Respectfully submitted,

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Dated:

4/3/02

SEQ ID NO:5 vs SEQ ID NO:1835



Q = CGI\_26caws20d648.seq

T = SEQ

A =

D = ID NO:1835

Identical Match = 282 Similar = 282 Total # Of Gaps = 41

Identity: Alignment = 54% Query = 11% Target = 54%

Similarity: Alignment = 54% Query = 11% Target = 54%

QS = 487 QE = 974 TS = 2 TE = 434

Q 487 AAAAACTTGAAATTTACAAGATAACGGA-AATGTTAAGAG-GAGA-AAGCTGATTGATT  
A A ACTT T TTAC GA AA GGA AAT TA GAG AGA AAG A T ATT  
T 2 AGATACTT----TGTACTTGAAAAAGGAGAATAATGAGTAAGACAAGAGCAGTTATT

Q 544 CACTTTAACTATGATAGAACATTATCAGTTATTG---CTGAAATAAAATCGAA--AAGC-  
C C TA T TGAT A ATTA CA TAT G CT A ATA AT GAA AAGC  
T 58 CCCGGTAGTTTGATCCA--ATTA-CA--TATGGTCACCTAGATATCATTGAAAGAAGCG

Q 598 CCATCTGTACCTCAATTACCGAACGTGATCTTGTCAACAAGTTAAAGATTATCAAAAA  
CC C G C T AT A C A GT TTGT A AA AAA A TA AAA  
T 113 CCGACCG--CTTGATGAAATCCATGT---TTGTGTACTAA--AAAATAGTAGTAAA--

Q 658 TATGGTGCTAATGCTATTCAATATTAACGTGATGAA--AAATACTTGGCGGTAGTTTG  
GGTG AA G TTT A T C GA GAA A AC TTG G AG T  
T 163 ---GGTG-GAACG---TTGACT----CAGAAGAACGCATGACGTTGATTGAAGAGT--

Q 716 AACGATTAATCAGTTATCAAAGATAACATCGTTACCAGTTATGAAAGAT--TTTAT  
CG TTAAA CA TT C AA AT ACA A CA TTT ATG A G T TT AT  
T 209 --CGGTTAAA-CATTTGCCTAATAT-ACAAGTCATCATTAAATGGATTGCTTGTGAT

Q 774 TATTGATAAAATTCAAATAGATGTTGCAAAACGAGCTGGTCATCTATTATTTA--TT  
T TTG A TCAA TA G TGCAA GA C ATTATT A TT  
T 265 TTTGTGA---TCAAGTA--GGTGCAA--GA-----CAATTATTCGAGGTT

Q 831 AATA---GTAAAT-ATTTAAGTGTGACCAATTAAAAGAATTGTATTGATATGCAACAA  
AA A GTAA T A TTT A T ATGA C A GA T TA T TATG AACAA  
T 306 AAGAGCTGTAAGTGACTTGAAT-ATGAAC----TACGACT--TACTTCTATG-AACAA

Q 887 ACCATAATTTAGAAGCTCTAGTAGAAGTTCATACAAT-TAGAGAACTTGA-ACGTGCACA  
A AA TTA A TAGTA A TT A ACAAT TA A A TGA A GTGCA A  
T 357 A---AAGTTAAA----TAGTA-ATATTGAAACAATGTACATGA--TGACAAGTGCAA

Q 945 CCA---AATTAACCTAAAATTATTGGTGTAA  
C A A TTA T AA TAT TGTTAA  
T 405 CTATTCATTTATAAGTTCAAGTAT---TGTTAA

EXHIBIT A

SEQ ID NO:6 vs SEQ ID NO:1835



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RANK 1 Score = 322.00 P\_Score = -1.0e+00

Q = CGI\_26cbws24d66a.seq

QF = D #Q Symbols = 8654

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 234 Similar = 234 Total # Of Gaps = 30

Identity: Alignment = 55% Query = 2% Target = 45%

Similarity: Alignment = 55% Query = 2% Target = 45%

QS = 2974 QE = 3380 TS = 62 TE = 429

|   |      |  |
|---|------|--|
| Q | 2974 | GTATTTGGAGTTCCCTCATATAATGATCTTTTCATA--ATTGTAATATTCTAACACTG<br>GTA TTT GA TCC TA A ATG TC TT ATA ATTG AA A A C C      |
| T | 62   | GTAGTTTGA--TCCAATTACATATGGTCACTTAGATATCATTGAAAGA---AGCGC-C   |
| Q | 3032 | GAGTGTAGTTAGATACTTGCTATGATTTTACTAAAAGTTTGGAGTTGCTCTAAAG<br>GA G TTT A A T C ATG TT T TACTAAAA A T GT TAAAG           |
| T | 115  | GACCGCTTGATGAAAT---CCATGTTGTACTAAAA-----AATAGTAGTAAAG  |
| Q | 3092 | TGGGAGTGTAGTAGAAAATAGCTGTTAAGAGGGGCTGTATACCAGTTG-TTGAAAGG<br>GT GAA T T CT AAGA GC TG AC GTTG TTGAA G                |
| T | 164  | -----GTGGAACGTTTGACTCAGAAGA-ACGCATG---AC--GTTGATTGAA--G  |
| Q | 3151 | AGTAATTTGGGC-TTG-CTTTTATA-GTTTTATATTTAATATCTTCTGTTTAGAA<br>AGT TT C TTTG CT TATA T AT TTTAAT T TG TT                 |
| T | 206  | AGTCGGTTAACATTCGCTAATATACAAGTGCATCATTAAATGGAT--TGCTT----   |
| Q | 3208 | GTTAATTT---AGAGAAAGTA-ATGTAACCTAAACTA--CAAGTTGTGAGA-ATGAAAAT<br>GTT ATTT GA AAGTA TG AA A AA TA C AG T T AGA TG AA T |
| T | 259  | GTTGATTTGTGATCAAGTAGGTGCAAAGACAATTATTCGAGGTTAAGAGCTGTAAGT  |
| Q | 3261 | GAATAGTAATGAAGAAATAACGA-TGCCTGCTGGTCATGGATGTTCACCTCATAATAT<br>GA T AAT A GAA T ACGA T TT TG CA A GTT A ATA TA        |
| T | 319  | GACTTTGAAT-ATGAACT-ACGACTTACTTCTATGAACA-AAAAGTTAA---ATAGTAA  |
| Q | 3320 | TATTGTGAGGTTATTACACTATTATTTAAATGAAATATTAATT-TAAAT--AAG<br>TATTG A A T TAC AT AT AA TG AA TATT ATTT TAA T AAG         |
| T | 372  | TATTGAAA---CAATGTAC---ATGATGACAAGTGCAAACATTCAATTATAAGTTCAAG  |
| Q | 3377 | CATT<br>ATT  |
| T | 426  | TATT   |

**EXHIBIT B**

SEQ ID NO:7 vs SEQ ID NO:1835

RANK 1 Score = 345.00 'P\_Score = -1.00  
Q = CGI\_26ccws22157d.seq QF = D #Q Symbols = 5024  
T = SEQ TF = D #T Symbols = 519

D = ID NO:1835

Identical Match = 156 Similar = 156 Total # Of Gaps = 17

Identity: Alignment = 56% Query = 3% Target = 30%

Similarity: Alignment = 56% Query = 3% Target = 30%

Similarity: Alignment = 33.00, query = 33, target = 33.

QS = 3068 QE = 3318 IS = 225 IE = 4/4

|   |      |                          |            |  |
|---|------|--------------------------|------------|--|
| Q | 3068 | TGATATAGAA               | ---        | CCCTTTTGATGTCTTATGATAAATTAAATAGACTTTGTAAAAAC |
|   |      | T ATATA AA               | C TTTT ATG | GAT TT T GA TTTTGT A AA                      |
| T | 225  | TAATATACAAGTGCATCTTAAATG | -----      | GATTGCTT-GTTGATTTTGTGATCAAG                  |

Q 3124 AAGCT--ATAGACAAAGTTGTTGCGAGGTGATATTATGAGTTATCA-TCACGAAGAAT  
AG T A AGACAA TT TT AGGT TTA GAG T T A T AC GAAT  
T 278 TAGGTGAAAGACAA----TTATTCGAGGT----TTAAGAGCTGTAAGTGA CTTTGAAT

Q 3181 ATG---ACATTTACATCAAAGGA-AACGATTTAACAGCTAATATTCAAGTAATAT-  
ATG AC TTAC TC A G A AA A TAA A TAATATT AA AAT T  
T 3229 ATGAACTTACGACTTAACTCTATGAGAAAGTTAATTA GTTAAATTGAGAGATGCT

|   |      |   |
|---|------|---|
| Q | 3235 | CAT-----TAAGAGCAAATCATT-ATTT-TAACCCCCGCAAAACACATAATAAACAAAGGG |
|   |      | CAT AAG GCAAA ATT ATTT TAA G AA T TAAA AAG                    |
| T | 387  | CATGATGACAAGTGCAAACATTCAATTATAA-----GTTCAAGTATTGTTAAAGAAGTA   |

|   |      |                                      |
|---|------|--------------------------------------|
| Q | 3288 | GAACCATATAAAG-----TATTTACCAAGTTTTATA |
|   |      | G CATAT AAG ATTT CA TTTT TA          |
| T | 442  | GCTGCATATCAAGCGGACATTT--CACCTTTGTAA  |

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## **EXHIBIT C**



RANK 1 Score = 288.00 P\_Score = -1.0e+00

Q = CGI\_26cdws332f0b.seq

QF = D #Q Symbols = 3287

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 233 Similar = 233 Total # Of Gaps = 29

Identity: Alignment = 55% Query = 7% Target = 44%

Similarity: Alignment = 55% Query = 7% Target = 44%

QS = 1617 QE = 2014 TS = 134 TE = 519

Q 1617 ATGTCAGGCTATCGAAATTATCAGTATTAA-GTGGA---CTGGCAAAAGAGAAC-CAT  
ATGT G TA C AAA AT AGTA T AA GTGGA TG C A AGAAC CAT

T 134 ATGTTTGTGTA-CTAAAAAAAT-AGTAGTAAAGGTGGAACGTTGACTCAGAAGAACGCAT

Q 1671 -TCTTGCGTTGCATTGTCGTGTAATTTGC---TATAGTGGCGTACCTCCTT  
C TTG TTG A GTCG AA TTTGC TATA GT C TC TTT

T 192 GACGTTG--ATTG-AAGAGTCGGTAAACATTGCCTAATATA---CAAGTGCATCATT

Q 1726 TAGTGGCTTCCGGTAAAGCTTAATATTCCA--AGGGGCTATTACAAATGTAATTAT  
TA TGG TT C G T A T TT T TC A AGG GC A ACAAA T ATT

T 246 TAATGGATTGCTTGTGA--TTTTGATCAAGTAGGTGCAAAGACAA---TTATTG

Q 1784 ATTGGTTAGCACTTATGATTGTGACAAGTTAATTGCTATGTA-TAGCTTTTAGAGT  
A GGTTTA A T T A GTGAC TTT A TATG A TA C TTA

T 300 A--GGTTTAAGAGCTGTA--GTGAC---TTTGA---ATATGAACTA--CGACTTACTTC

Q 1843 GATGTTATAATGTATTTGGTGATGCTGACGGAGAACAA-GTACAATTTAGACCA---C  
ATG A AA GT T GT AT TGA AACAA GTAC AT GAC A C

T 348 TATGAACAAAAGTTAAATAGTAATATTGA----AACAAATGTAC-ATGATGACAAGTGC

Q 1899 TACCTATTTATCGTAAAGTTACTTAGTGTGTTAGTTAGTGGTATTAGCGA-TGGGT  
A CTATT AT TA A GTT A TA TGTT AG GTAG G A TA C A GG

T 402 AAACATTCA-TTATAAGTTCAAGTATTGTTAAAGAAGTAGCTGCA-TATCAAGCGGAC

Q 1958 ATTGCAGCCCTGTTGT---TCTGAAAGTAACAGAGGATGCAACA--AATCTTAATATG  
ATT CA CCT TTGT CT A A AGAG AT AA A AA TTAAT T

T 460 ATTTCA---CCTTTGTACCACTCATGTCGAAAGAGCATTAAAAAGAAATTAAATGTT

Q 2012 AAA

AA

T 517 TAA

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CLAIMS

5 1. (Amended) An isolated nucleic acid comprising a nucleotide sequence  
encoding an *S. epidermidis* polypeptide ~~selected from the group consisting of~~ SEQ ID  
NO: 3773—SEQ ID NO: 75445607.

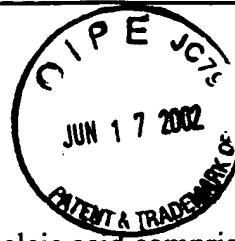
10 5. (Amended) An isolated nucleic acid comprising a nucleotide sequence  
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues  
~~thereof, said nucleic acid selected from the group consisting of~~ SEQ ID NO: 1835—SEQ  
ID NO: 3772.

15 9. (Amended) A probe comprising a nucleotide sequence consisting of at least  
fortyeight contiguous nucleotides of a nucleotide sequence ~~selected from the group~~  
~~consisting of~~ SEQ ID NO: 1—SEQ ID NO: 37721835.

20 10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at  
least eight—forty nucleotides in length, wherein the sequence is hybridizable to a nucleic  
acid having a nucleotide sequence ~~selected from the group consisting of~~ SEQ ID NO: 1—  
SEQ ID NO: 37721835.

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CLAIMS



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5        1. (Amended) An isolated nucleic acid comprising a nucleotide sequence  
encoding an *S. epidermidis* polypeptide of SEQ ID NO:5607.

5. (Amended) An isolated nucleic acid comprising a nucleotide sequence  
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues ,  
10      said nucleic acid of SEQ ID NO:1835.

9. (Amended) A probe comprising a nucleotide sequence consisting of at least  
forty contiguous nucleotides of a nucleotide sequence of SEQ ID NO:1835.

15      10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at  
least forty nucleotides in length, wherein the sequence is hybridizable to a nucleic acid  
having a nucleotide sequence of SEQ ID NO: 1835.